

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:40:12, Search time 40.0714 seconds  
(without alignments)  
56.562 Million cell updates/sec

Title: US-09-856-070-23  
Perfect score 55  
Sequence: 1 ELMRLQDYEE 11

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_orquanelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rviro:\*
- 16: sp\_bacterioph:\*
- 17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	55	100.0	586	4 Q96C08	Q96C08 homo sapien
2	52	94.5	159	4 Q9UJ26	Q9UJ26 homo sapien
3	52	94.5	586	11 Q9F711	Q9F711 mus musculu
4	50	90.9	158	4 Q9UJ27	Q9UJ27 homo sapien
5	48	87.3	455	11 Q8VHF3	Q8VHF3 rattus norv
6	40	72.7	585	13 Q9VQW6	Q9VQW6 gallus gall
7	39	70.9	429	4 P78514	P78514 homo sapien
8	39	70.9	453	4 Q99854	Q99854 homo sapien
9	39	70.9	634	9 Q9X7S3	Q9X7S3 bacterioph
10	39	70.9	802	4 Q9Y699	Q9Y699 homo sapien
11	38	69.1	130	16 Q9K660	Q9K660 bacillus ba
12	38	69.1	150	16 Q8UHF2	Q8UHF2 agrobacteri
13	37	67.3	111	9 Q64106	Q64106 bacterioph
14	37	67.3	111	16 Q34838	Q34838 bacillus su
15	37	67.3	217	17 Q80102	Q80102 pyrococcus
16	37	67.3	231	17 Q8U0V8	Q8U0V8 pyrococcus

17	37	67.3	292	5 Q8T9V0	Q8T9V0 aedes aegypt
18	37	67.3	321	16 Q9P0S2	Q9P0S2 xylella las
19	37	67.3	337	16 Q66941	Q66941 aquifex aco
20	37	67.3	1058	13 Q91480	Q91480 salmo salar
21	36	65.5	250	16 Q9H742	Q9H742 pseudomonas
22	36	65.5	284	10 Q92301	Q92301 arabidopsis
23	36	65.5	338	16 Q9FAP4	Q9FAP4 xylella las
24	36	65.5	454	13 Q57748	Q57748 xenopus lae
25	35	63.6	66	16 Q9K728	Q9K728 bacillus ba
26	35	63.6	151	16 Q9K191	Q9K191 streptomyces
27	35	63.6	221	16 Q97FF3	Q97FF3 clostridium
28	35	63.6	246	5 Q8SV08	Q8SV08 encephalito
29	35	63.6	256	16 Q8PCX7	Q8PCX7 thermococcus
30	35	63.6	418	5 Q8T3H6	Q8T3H6 drosophila
31	35	63.6	443	5 Q9VPI8	Q9VPI8 drosophila
32	35	63.6	477	10 Q81465	Q81465 arabidopsis
33	35	63.6	534	13 Q90XY5	Q90XY5 fugu rubrip
34	35	63.6	754	13 Q98U16	Q98U16 cyprinus ca
35	35	63.6	892	4 Q9BTN1	Q9BTN1 homo sapien
36	35	63.6	1298	10 Q9LSA4	Q9LSA4 arabidopsis
37	34	61.8	105	17 Q29591	Q29591 archaevoglob
38	34	61.8	150	10 Q94H91	Q94H91 oryza sativ
39	34	61.8	181	10 Q91777	Q91777 oryza sativ
40	34	61.8	186	10 Q94F17	Q94F17 arabidopsis
41	34	61.8	235	11 Q9D5Q0	Q9D5Q0 mus musculu
42	34	61.8	250	17 Q9HK00	Q9HK00 halobacteri
43	34	61.8	294	11 Q9P058	Q9P058 mus musculu
44	34	61.8	314	11 Q9P057	Q9P057 mus musculu
45	34	61.8	321	10 Q91KM6	Q91KM6 zea mays (m

ALIGNMENTS

RESULT 1  
Q96C08  
ID Q96C08 PRELIMINARY: PRT: 586 AA.  
AC Q96C08  
DI 01-DEC-2001 (TREMBL) 19, Created)  
DT 01-DEC-2001 (TREMBL) 19, last sequence update)  
DT 01-MAR-2002 (TREMBL) 20, last annotation update)  
DE Similar to villin 2 (ezrin).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
PL Submitted (Sep 2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL: AC013903; AAI13903.1; .  
DR InterPro: IPR000299; Band.4.1.  
DR InterPro: IPR000798; Ez/rad/moesin.  
DR Pfam: PF00373; Band.4.1; 1.  
DR Pfam: PF00760; ERM; 1.  
DR PROSITE: PS00660; BAND\_4\_1; UNKNOWN.1.  
DR PROSITE: PS00661; BAND\_4\_2; UNKNOWN.1.  
DR PROSITE: PS00662; BAND\_4\_3; 1.  
SQ SEQUENCE 586 AA: 69412 MW: 116592.49A:3546 QK664;  
Query Match 100.0%; Score 55; DB 4; Length 586;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 11; Conservative 0; Mismatches 0; Indels 6; Gaps 0;

QV 1 ELMRLQDYEE 11  
|||  
DQ 346 ELMRLQDYEE 356

RESULT 2  
Q9UJ26  
ID Q9UJ26 PRELIMINARY: PRT: 159 AA.

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AC Q90J26;
DT 01 MAY-2000 (TEMBLrel. 13, Created)
DT 01 MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01 MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fadiel A., Chen Z.C., Nattoli F.;
RL "Mutation of ezrin gene in cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189213; AAF03156.1; -.
DR InterPro: IPR000299; Hand_4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 19234 MW; 7C398388B7A70FA CRC64;

Query Match 94.5%; Score 52; DB 4; Length 159;
Best Local Similarity 90.9%; Pred. No. 0.034;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYDE 11
ID 149 ELMRLQDYDE 159
DB 149 ELMRLQDYDE 159

RESULT 3
Q90J11
ID Q90J11 PRELIMINARY; PRI: 586 AA.
AC Q90J11;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Adult male kidney cDNA, RIKEN full-length enriched library,
DE clone-0610047R22, full insert sequence.
CN VIL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6J; TISSUE-KIDNEY;
RA MEDLINE 21085660; PubMed 11217851;
RA Kawai J., Shindagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hata A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka T.,
RA Saito T., Okazaki Y., Gotohori T., Pogo H., Kasukawa T., Saito R.,
RA Kudota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleisermann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirra L.M., Stanbly F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Haldarelli R., Harsh G.,
RA Blake J., Bellelli D., Benjuna N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Holtmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilting L.,
RA Wyushaw-Horiz A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA Bayashizaki Y.;
RI "Functional annotation of a full-length mouse cDNA collection.";
RC Nature 409:685-690(2001).
DR EMBL: AK02766; BAB2341.1; -.
DR MGD: MGI:98941; Vil2.
DR InterPro: IPR000299; Band_4.1.

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DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00373; Band_41; 1.
DR Pfam: PF00769; ERM; 1.
DR PRINTS: PR00935; HAND41.
DR SMART: SMO0295; B41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
SQ SEQUENCE 586 AA; 69434 MW; 591A88F575F6DE3E CRC64;

Query Match 94.5%; Score 52; DB 11; Length 586;
Best Local Similarity 90.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYDE 11
ID 346 ELMRLQDYDE 356
DB 346 ELMRLQDYDE 356

RESULT 4
Q90J27
ID Q90J27 PRELIMINARY; PRI: 158 AA.
AC Q90J27;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen Z.C., Fadiel A., Nattoli F.;
RL "Ezrin gene mutation in ovarian cancer.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF188897; AAF03155.1; -.
DR InterPro: IPR000299; Hand_4.1.
DR InterPro: IPR000798; Ez/rad/moesin.
DR Pfam: PF00769; ERM; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 158
SQ SEQUENCE 158 AA; 19089 MW; 86F92E1BC6F2957E CRC64;

Query Match 90.9%; Score 50; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYDE 10
ID 149 ELMRLQDYDE 158
DB 149 ELMRLQDYDE 158

RESULT 5
Q8VHK3
ID Q8VHK3 PRELIMINARY; PRI: 455 AA.
AC Q8VHK3;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Ezrin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-SPRAGUE-DAWLEY;
RA Gunn-Moore F.J., Tait S., Murphy P.J.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF450298; AAL47844.1; -.

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DP InterPro: IPR000294; Band 4 1  
 DR InterPro: IPR000794; E2/rad/moesin.  
 DR Pfam: PF00373; Band 41; 1.  
 DR Pfam: PF00769; ERM; 1.  
 DR PRINTS: PR00935; BAND41.  
 DR SMART: SM00295; R41; 1.  
 DR PROSITE: PS00660; BAND\_41\_1; UNKNOWN\_1.  
 DR PROSITE: PS00661; BAND\_41\_2; UNKNOWN\_1.  
 DR PROSITE: PS00661; BAND\_41\_3; 1.  
 DR PROSITE: PS00661; BAND\_41\_3; 1.  
 FT NON\_TER 455  
 SQ SEQUENCE 455 AA; 54174 MW; 1FC9A95F4C7D5893 CRC64.

Query Match 87.3% Score 48; DB 13; Length 455;  
 Best Local Similarity 81.8%; Pred. No. 0.58;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11

|||||||

DB 346 ELMRLQDYEE 356

RESULT 6

Q9YGW6

ID Q9YGW6 PRELIMINARY; PRT; 585 AA.

AC Q9YGW6;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DI 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Ezrin.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LEGHORN; TISSUE-BRAIN;

EX MEDLINE-99171943; PubMed-10051754;

RA Takahashi M., Yamada M., Noda M.;

RT "Specific expression of ezrin, a cytoskeletal membrane linker protein,

in a subset of chick retinotectal and sensory projections".

RL Eur. J. Neurosci. 11:545-558(1999).

DR EMBL: AB019790; BAA75497.1; -.

DR InterPro: IPR000299; Band 4 1.

DR InterPro: IPR000794; E2/rad/moesin.

DR Pfam: PF00373; Band 41; 1.

DR Pfam: PF00769; ERM; 1.

DR PRINTS: PR00935; BAND41.

DR SMART: SM00295; R41; 1.

DR PROSITE: PS00660; BAND\_41\_1; 1.

DR PROSITE: PS00661; BAND\_41\_2; 1.

DR PROSITE: PS00661; BAND\_41\_3; 1.

SQ SEQUENCE 585 AA; 69366 MW; 854C6348F7A3C49C CRC64;

Query Match 72.7% Score 40; DB 13; Length 585;

Best Local Similarity 70.0%; Pred. No. 25;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 10

|||||||

DB 346 ELLVRLQYEE 355

RESULT 7

P78514

ID P78514 PRELIMINARY; PRT; 429 AA.

AC P78514;

DI 01-MAY-1997 (TrEMBLrel. 03, Created)

DI 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DI 01-MAY-1997 (TrEMBLrel. 03, Last annotation update)

DE Hypothetical 48.1 kDa protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RA Keen T.J.;

KL Submitted (JUL 1997) to the EMBL/GenBank/DBJ databases.

DP EMBL: U85994; AAR61919.1; -.

DR EMBL: U85994; AAR61918.1; -.

DR EMBL: U85997; AAR46606.1; -.

KW Hypothetical protein.

FT NON\_TER 1

SQ SEQUENCE 429 AA; 48892 MW; D6E347A95971E9A CRC64;

Query Match 70.9% Score 39; DB 4; Length 429;

Best Local Similarity 72.7%; Pred. No. 29;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11

|||||||

DB 157 ELLVRLQYEE 167

RESULT 8

Q99854

ID Q99854 PRELIMINARY; PRT; 453 AA.

AC Q99854;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DI 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical 51.1 kDa protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-SPLEEN;

RA Keen T.J.;

KL Submitted (JAN 1997) to the EMBL/GenBank/DBJ databases.

DP EMBL: U87408; AAB47568.1; -.

KW Hypothetical protein.

FT NON\_TER 1

SQ SEQUENCE 453 AA; 51050 MW; C5F53E164A83D418 CRC64;

Query Match 70.9% Score 39; DB 4; Length 453;

Best Local Similarity 72.7%; Pred. No. 30;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11

|||||||

DB 181 ELLVRLQYEE 191

RESULT 9

Q9AJS3

ID Q9AJS3 PRELIMINARY; PRT; 634 AA.

AC Q9AJS3;

DI 01-NOV-1999 (TrEMBLrel. 12, Created)

DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Putative replication initiation protein p12.

OS Bacteriophage PM2.

OC Viruses; dsDNA viruses, no RNA stage; Corticoviridae; Corticovirus.

OX NCBI\_TaxID=10661;

RN [1]

RP SEQUENCE FROM N.A.

RA Kivela H.M., Mannisto E.H., Kalkinen N., Bamford D.H.;

RT "Purification and protein composition of PM2, the first lipid-

containing bacterial virus to be isolated.";

PL Virology 0:0-0(1999).

RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE-99434246; PubMed-10502514;
KA Mannisto R.H., Kivela H.M., Paulin L., Bamford D.H., Bamford J.K.;
RI "The complete genome sequence of PM2, the first lipid containing
RT bacterial virus to be isolated.";
RL Virology 262:355-363(1999).
RN [1]
RP SEQUENCE FROM N.A.
KA Mannisto R.H., Kivela H.M., Paulin L., Bamford D.H., Bamford J.K.H.;
RL Submitted (MAY 1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF155037; A043543.1; -.
SQ SEQUENCE 634 AA; 72894 MW; 4F5CDB0004FF02506 CRC64;

Query Match 70.9%; Score 39; DB 9; Length 634;
Best local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 275 ELMVRIQYEE 285
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|111111|

RESULT 10
QY699 PRELIMINARY: PPT: 802 AA.
AC QY699;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DE Transcriptional regulator, AsnC family.
GN AT00740 OR AGR_C_1339.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
KA TISSUE-OSTEOSARCOMA;
RX MEDLINE-99246731; PubMed-10221542;
KA Adams A.E., Rosenblatt M., Suva L.J.;
RT "Identification of a novel parathyroid hormone responsive gene in
RI human osteoblastic cells.";
RL Bone 24:305-313(1999).
DR EMBL: AF095771; A025981.1; -.
SQ SEQUENCE 802 AA; 89844 MW; 3D7B534492C4CA92 CRC64;

Query Match 70.9%; Score 39; DB 4; Length 802;
Best local Similarity 72.7%; Pred. No. 54;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 540 ELMRLQDYEE 540
|||||
|111111|

RESULT 11
QY660 PRELIMINARY: PPT: 130 AA.
AC QY660;
DT 01-001-2000 (TEMBLrel. 15, Created)
DT 01-001-2000 (TEMBLrel. 15, Last sequence update)
DE Hypothetical protein BH3872.
GN BH3872.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group, Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
KA STRAIN-C-125 / JCM 9154;
RX MEDLINE-20512582; PubMed-11058132;
KA Takami H., Nakasone K., Takaki Y., Mado G., Sasaki R., Masui N.,

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RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,
KA Horikoshi K.;
RI "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001520; HA07591.1; -.
DR InterPro: IPR004360; Gly_bico_diox.
DR Pfam: PF00903; Glyoxalase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 130 AA; 15271 MW; B39FE8EED72DF09F CRC64;

Query Match 69.1%; Score 38; DB 16; Length 130;
Best local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LRLODYEE 11
DB 78 LRVDYEE 85
|||||
|111111|

RESULT 12
QY80HE2 PRELIMINARY: PPT: 150 AA.
AC QY80HE2;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Transcriptional regulator, AsnC family.
GN AT00740 OR AGR_C_1339.
OS Agrobacterium tumefaciens (strain C58 / ATCC 34970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
KA MEDLINE-21608550; PubMed-11743193;
KA Wood D.W., Setubal J.C., Kaul P., Monks D.F., Kitajima J.P.,
KA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
KA Chen Y., Falsen I.T., Eisen J.A., Karp P.D., Boyee D., Sr.,
KA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
KA Kutayian T., Levy K., Li M.-J., McLelland E., Palmieri A.,
KA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
KA Zhang S., You H., Tao Y., Hiddle P., Jung M., Krespan W., Perry M.,
KA Gordon-Kamm R., Liang L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
KA Chumley F., Tinney S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
KA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RI C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21608551; PubMed-11743194;
KA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
KA Quorillo H., Goldman H.S., Cao Y., Askenazi M., Halling C., Mullin L.,
KA Houmlel K., Gordon J., Vaudin M., Jarchook O., Ppp A., Liu F.,
KA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz H.,
KA Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
KA Clelo C., Slater S.;
RI "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL: AF009042; A041756.1; -.
DR EMBL: AE008008; A0486548.1; -.
KW Complete proteome.
SQ SEQUENCE 150 AA; 16748 MW; 4BE5AR39E46125FD CRC64;

Query Match 69.1%; Score 38; DB 16; Length 150;
Best local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMLRLQDYEE 11
DB 106 LMLRLQDYEE 115
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|111111|

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RESULT 13
ID 064106 PRELIMINARY: PPT: 111 AA
AC 064106
DT 01-AUG-1998 (TREMblrel. 07, Created)
DI 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 10, Last annotation update)
DE Hypothetical 12.5 kDa protein.
GN YOPW.
OS Bacteriophage SPK2.
OC VIRUSES; dsDNA viruses, no RNA stage, Caudovirales; Siphoviridae.
OX NCBI_TaxID=66797;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Mauei C.,
RA Karamata D.;
RT "the complete nucleotide sequence of the Bacillus subtilis SPK2
RT prophage.";
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases
DR EMBL: AF029913; AF013066.1;
KW Hypothetical protein.
SQ SEQUENCE 111 AA; 12549 MW; F1886HRC44AF78 CRC64;

Query Match 67.3%; Score 37; DB 9; Length 111;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 20 EKLKLSIDYEE 30
IIII:IIII

RESULT 14
Q34838
ID 034838 PRELIMINARY: PPT: 111 AA.
AC 034838
DT 01-JAN-1998 (TREMblrel. 05, Created)
DI 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DI 01-MAR-2002 (TREMblrel. 10, Last annotation update)
DE YOPW protein.
GN YOPW.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunz F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Becker M.G., Bessieres P., Bolotin A., Borchert S.,
RA Horst R., Houtsier L., Brans A., Braun M., Brignell S.C., Hron S.,
RA Brouillet S., Bruschi C.V., Caldwell R., Capuano V., Carter N.M.,
RA Choi S.K., Cudani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Eulian K.D., Errington J., Fabre C., Ferrarini A., Fougere D.,
RA Fritz G., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi C.,
RA Gutseppe G., Guy H.J., Haga K., Haeck J., Harwood C.R., Hebaoui A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koehler P., Konopyskein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauei C., Medigue V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neuge B., O'Keilly M., Ogilawa K., Ogilawa K., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescran E., Puig P., Purcell R., Rappoport G., Roy M., Rylands S.,
RA Rieger M., Rivilla C., Roche E., Roche P., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Scheich S., Schroeter R., Scofield F.,
RA Sekiguchi J., Skowska A., Soror S.J., Serror P., Shin H.S., Soldo B.,

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RA Sorokin A., Taroni E., Takagi T., Takabashi H., Takemaru K.,
RA Takeuchi M., Yamakoshi A., Tanaka T., Terpstra P., Iodoni A.,
RA Tetsuo V., Uchiyama S., Vandenbol M., Vardier F., Vassarotti A.,
RA Viari A., Wambull R., Wedler E., Wedler H., Weizenecker T.,
RA Winters P., Wipit A., Yamamoto H., Yamane K., Yamamoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.;
RT "the complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RN [2]
RP Nature 390:249-256(1997).
RC SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunz F., Ogasawara N., Yoshikawa H., Zanchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z99114; CAB13966.1;
DR EMBL: Z99115; CAB13992.1;
KW Complete proteome.
SQ SEQUENCE 111 AA; 12549 MW; F1886HRC44AF78 CRC64;

Query Match 67.3%; Score 37; DB 16; Length 111;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 20 EKLKLSIDYEE 30
IIII:IIII

RESULT 15
Q80102
ID Q80102 PRELIMINARY: PPT: 217 AA.
AC Q80102
DT 01-JUN-2002 (TREMblrel. 21, Created)
DI 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DI 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical protein PF1113.
GN PF1113.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae; Thermococcaceae;
OX Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VCL / DSM 1638 / ATCC 43587 / JCM 8422;
RA Weiss P., Dunn P.M., Robb F.I., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF010221; AAL81237.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 217 AA; 24508 MW; 91F253HF57C38451 CRC64.

Query Match 67.3%; Score 37; DB 17; Length 217;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
DB 169 EIVPFLDYEE 179
IIII:IIII

Search completed, January 16, 2003, 16:55:45
Job time : 41.0714 secs

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